

SEQUENCE LISTING

<110> Schmaljohn, Connie S.
Fuller, James T.

<120> Nucleic Acid Immunization

<130> 033267-021

<140> US 10/411,205

<141> 2003-04-11

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> CpG dinucleotides

<400> 1

tcctgacgt tcctgatgct

20

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotides which comprise CpG
motifs

<400> 2

atcgactctc gagcgttctc

20

<210> 3

<211> 2605

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (174) ... (2465)

<400> 3

ggatcctttt ctattaaaca tataaattct tttttatggt atataatttat aaaagttctg 60
tttaaaaagc caaaaataaa taattatctc tttttattta tattatattg aaactaaagt 120
ttattaattt caatataata taaatttaat tttatacaaa aaggagaacg tat atg 176
Met
1

aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata tta 224
Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile Leu
5 10 15

gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa cag	272
Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys Gln	
20 25 30	
gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta cta	320
Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu Leu	
35 40 45	
gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt acc	368
Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val Thr	
50 55 60 65	
tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa aat	416
Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu Asn	
70 75 80	
att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga ttt	464
Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly Phe	
85 90 95	
atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct gat	512
Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala Asp	
100 105 110	
aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa gct	560
Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys Ala	
115 120 125	
tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa ata	608
Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln Ile	
130 135 140 145	
aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat ttc	656
Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp Phe	
150 155 160	
aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct agt	704
Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser Ser	
165 170 175	
gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca aga	752
Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser Arg	
180 185 190	
aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac aat	800
Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp Asn	
195 200 205	
gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat gtc	848
Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp Val	
210 215 220 225	
aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat gaa	896
Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His Glu	
230 235 240	
aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc acg	944
Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser Thr	

				245				250				255							
gct	tct	gat	ccg	tac	agt	gat	ttc	gaa	aag	gtt	aca	gga	cgg	att	gat	992			
Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	Glu	Lys	Val	Thr	Gly	Arg	Ile	Asp				
		260				265						270							
aag	aat	gta	tca	cca	gag	gca	aga	cac	ccc	ctt	gtg	gca	gct	tat	ccg	1040			
Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	His	Pro	Leu	Val	Ala	Ala	Tyr	Pro				
		275				280						285							
att	gta	cat	gta	gat	atg	gag	aat	att	att	ctc	tca	aaa	aat	gag	gat	1088			
Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu	Ser	Lys	Asn	Glu	Asp				
290				295						300				305					
caa	tcc	aca	cag	aat	act	gat	agt	gaa	acg	aga	aca	ata	agt	aaa	aat	1136			
Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg	Thr	Ile	Ser	Lys	Asn				
				310						315				320					
act	tct	aca	agt	agg	aca	cat	act	agt	gaa	gta	cat	gga	aat	gca	gaa	1184			
Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	Gly	Asn	Ala	Glu				
		325						330				335							
gtg	cat	gcg	tcg	ttc	ttt	gat	att	ggg	ggg	agt	gta	tct	gca	gga	ttt	1232			
Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser	Val	Ser	Ala	Gly	Phe				
		340				345						350							
agt	aat	tcg	aat	tca	agt	acg	gtc	gca	att	gat	cat	tca	cta	tct	cta	1280			
Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp	His	Ser	Leu	Ser	Leu				
		355				360						365							
gca	ggg	gaa	aga	act	tgg	gct	gaa	aca	atg	ggg	tta	aat	acc	gct	gat	1328			
Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly	Leu	Asn	Thr	Ala	Asp				
370				375						380				385					
aca	gca	aga	tta	aat	gcc	aat	att	aga	tat	gta	aat	act	ggg	acg	gct	1376			
Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	Thr	Gly	Thr	Ala				
				390				395				400							
cca	atc	tac	aac	gtg	tta	cca	acg	act	tcg	tta	gtg	tta	gga	aaa	aat	1424			
Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	Leu	Gly	Lys	Asn				
		405				410						415							
caa	aca	ctc	gcg	aca	att	aaa	gct	aag	gaa	aac	caa	tta	agt	caa	ata	1472			
Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	Leu	Ser	Gln	Ile				
		420				425						430							
ctt	gca	cct	aat	aat	tat	tat	cct	tct	aaa	aac	ttg	gcg	cca	atc	gca	1520			
Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn	Leu	Ala	Pro	Ile	Ala				
		435				440				445									
tta	aat	gca	caa	gac	gat	ttc	agt	tct	act	cca	att	aca	atg	aat	tac	1568			
Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro	Ile	Thr	Met	Asn	Tyr				
450				455						460				465					
aat	caa	ttt	ctt	gag	tta	gaa	aaa	acg	aaa	caa	tta	aga	tta	gat	acg	1616			
Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln	Leu	Arg	Leu	Asp	Thr				
				470				475						480					
gat	caa	gta	tat	ggg	aat	ata	gca	aca	tac	aat	ttt	gaa	aat	gga	aga	1664			

Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	Glu	Asn	Gly	Arg		
			485					490					495				
gtg	agg	gtg	gat	aca	ggc	tcg	aac	tgg	agt	gaa	gtg	tta	ccg	caa	att	1712	
Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	Leu	Pro	Gln	Ile		
		500					505					510					
caa	gaa	aca	act	gca	cgt	atc	att	ttt	aat	gga	aaa	gat	tta	aat	ctg	1760	
Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	Asp	Leu	Asn	Leu		
	515					520					525						
gta	gaa	agg	cgg	ata	gcg	gcg	gtt	aat	cct	agt	gat	cca	tta	gaa	acg	1808	
Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	Pro	Leu	Glu	Thr		
530					535					540					545		
act	aaa	ccg	gat	atg	aca	tta	aaa	gaa	gcc	ctt	aaa	ata	gca	ttt	gga	1856	
Thr	Lys	Pro	Asp	Met	Thr	Leu	Lys	Glu	Ala	Leu	Lys	Ile	Ala	Phe	Gly		
				550					555					560			
ttt	aac	gaa	ccg	aat	gga	aac	tta	caa	tat	caa	ggg	aaa	gac	ata	acc	1904	
Phe	Asn	Glu	Pro	Asn	Gly	Asn	Leu	Gln	Tyr	Gln	Gly	Lys	Asp	Ile	Thr		
			565					570					575				
gaa	ttt	gat	ttt	aat	ttc	gat	caa	caa	aca	tct	caa	aat	atc	aag	aat	1952	
Glu	Phe	Asp	Phe	Asn	Phe	Asp	Gln	Gln	Thr	Ser	Gln	Asn	Ile	Lys	Asn		
		580					585					590					
cag	tta	gcg	gaa	tta	aac	gca	act	aac	ata	tat	act	gta	tta	gat	aaa	2000	
Gln	Leu	Ala	Glu	Leu	Asn	Ala	Thr	Asn	Ile	Tyr	Thr	Val	Leu	Asp	Lys		
	595					600					605						
atc	aaa	tta	aat	gca	aaa	atg	aat	att	tta	ata	aga	gat	aaa	cgt	ttt	2048	
Ile	Lys	Leu	Asn	Ala	Lys	Met	Asn	Ile	Leu	Ile	Arg	Asp	Lys	Arg	Phe		
610					615					620					625		
cat	tat	gat	aga	aat	aac	ata	gca	gtt	ggg	gcg	gat	gag	tca	gta	gtt	2096	
His	Tyr	Asp	Arg	Asn	Asn	Ile	Ala	Val	Gly	Ala	Asp	Glu	Ser	Val	Val		
				630					635					640			
aag	gag	gct	cat	aga	gaa	gta	att	aat	tcg	tca	aca	gag	gga	tta	ttg	2144	
Lys	Glu	Ala	His	Arg	Glu	Val	Ile	Asn	Ser	Ser	Thr	Glu	Gly	Leu	Leu		
			645					650					655				
tta	aat	att	gat	aag	gat	ata	aga	aaa	ata	tta	tca	ggt	tat	att	gta	2192	
Leu	Asn	Ile	Asp	Lys	Asp	Ile	Arg	Lys	Ile	Leu	Ser	Gly	Tyr	Ile	Val		
		660					665					670					
gaa	att	gaa	gat	act	gaa	ggg	ctt	aaa	gaa	gtt	ata	aat	gac	aga	tat	2240	
Glu	Ile	Glu	Asp	Thr	Glu	Gly	Leu	Lys	Glu	Val	Ile	Asn	Asp	Arg	Tyr		
	675					680					685						
gat	atg	ttg	aat	att	tct	agt	tta	cgg	caa	gat	gga	aaa	aca	ttt	ata	2288	
Asp	Met	Leu	Asn	Ile	Ser	Ser	Leu	Arg	Gln	Asp	Gly	Lys	Thr	Phe	Ile		
690					695					700					705		
gat	ttt	aaa	aaa	tat	aat	gat	aaa	tta	ccg	tta	tat	ata	agt	aat	ccc	2336	
Asp	Phe	Lys	Lys	Tyr	Asn	Asp	Lys	Leu	Pro	Leu	Tyr	Ile	Ser	Asn	Pro		
				710					715					720			

aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att att 2384
 Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile Ile
 725 730 735

aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa att 2432
 Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys Ile
 740 745 750

tta atc ttt tct aaa aaa ggc tat gag ata gga taaggtaatt ctaggtgatt 2485
 Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 755 760

tttaaattat ctaaaaaaca gtaaaattaa aacataactct ttttgtaaga aatacaagga 2545
 gagtatgttt taaacagtaa tctaaatcat cataatcctt tgagattggt tgtaggatcc 2605

<210> 4

<211> 764

<212> PRT

<213> Bacillus anthracis

<400> 4

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
 1 5 10 15
 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys
 20 25 30
 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
 35 40 45
 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
 50 55 60
 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
 65 70 75 80
 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
 85 90 95
 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
 100 105 110
 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
 115 120 125
 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
 130 135 140
 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
 145 150 155 160
 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
 165 170 175
 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
 180 185 190
 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
 195 200 205
 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
 210 215 220
 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
 225 230 235 240
 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
 245 250 255
 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
 260 265 270
 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
 275 280 285
 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu

290	295	300													
Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys															
305	310	315													320
Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala															
	325	330													335
Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly															
	340	345													350
Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser															
	355	360													365
Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala															
	370	375													380
Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr															
385	390	395													400
Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys															
	405	410													415
Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln															
	420	425													430
Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile															
	435	440													445
Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn															
	450	455													460
Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp															
465	470	475													480
Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly															
	485	490													495
Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln															
	500	505													510
Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn															
	515	520													525
Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu															
	530	535													540
Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe															
545	550	555													560
Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile															
	565	570													575
Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys															
	580	585													590
Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp															
	595	600													605
Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg															
	610	615													620
Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val															
625	630	635													640
Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu															
	645	650													655
Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile															
	660	665													670
Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg															
	675	680													685
Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe															
	690	695													700
Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn															
705	710	715													720
Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile															
	725	730													735
Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys															
	740	745													750
Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly															
	755	760													

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward PCR primer

<400> 5
 gtcagctagc gaggtgattc aggcagaagt t 31

<210> 6
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse PCR primer

<400> 6
 cagtgcctagc tcctatctca tagcc 25

<210> 7
 <211> 66
 <212> DNA
 <213> Homo sapiens

<400> 7
 atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcggt 60
 tcggct 66

<210> 8
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Ala
 20